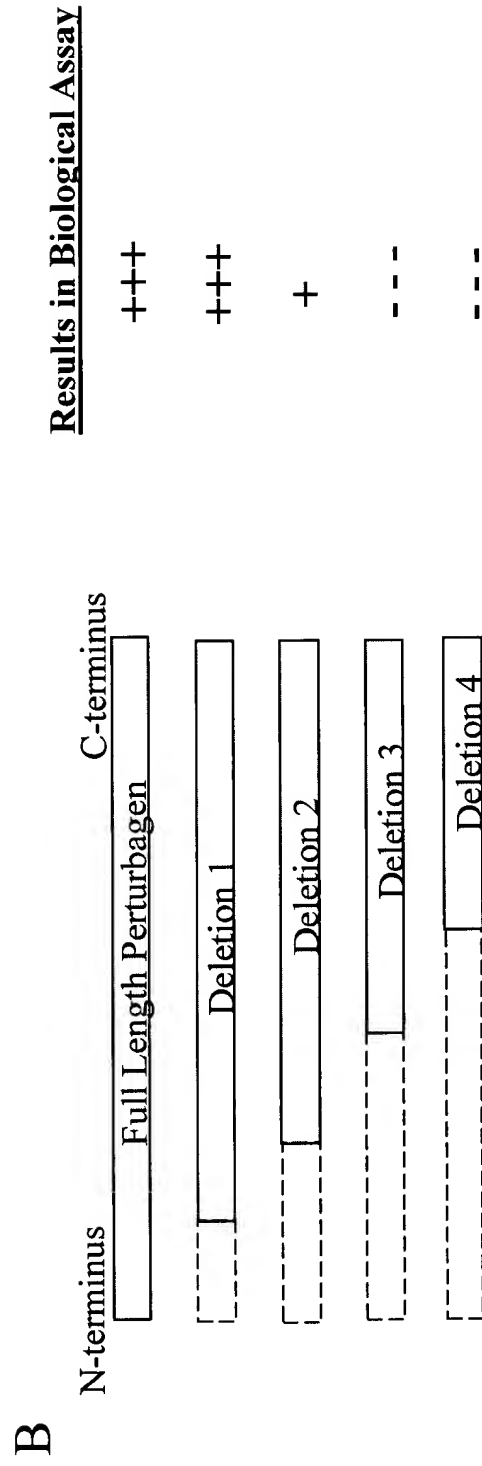
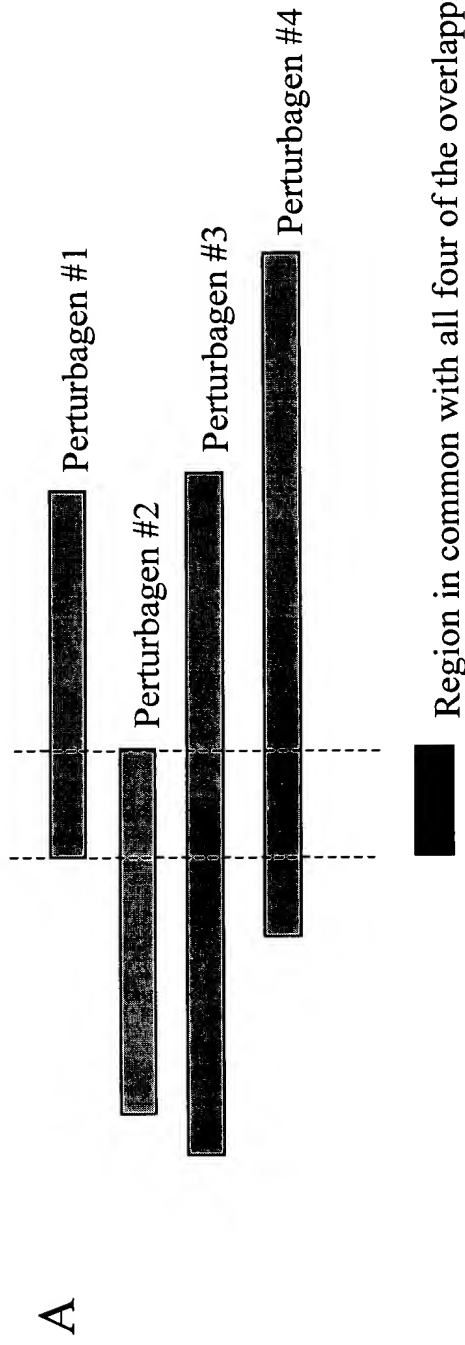


Figure 1

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**Figure 2**

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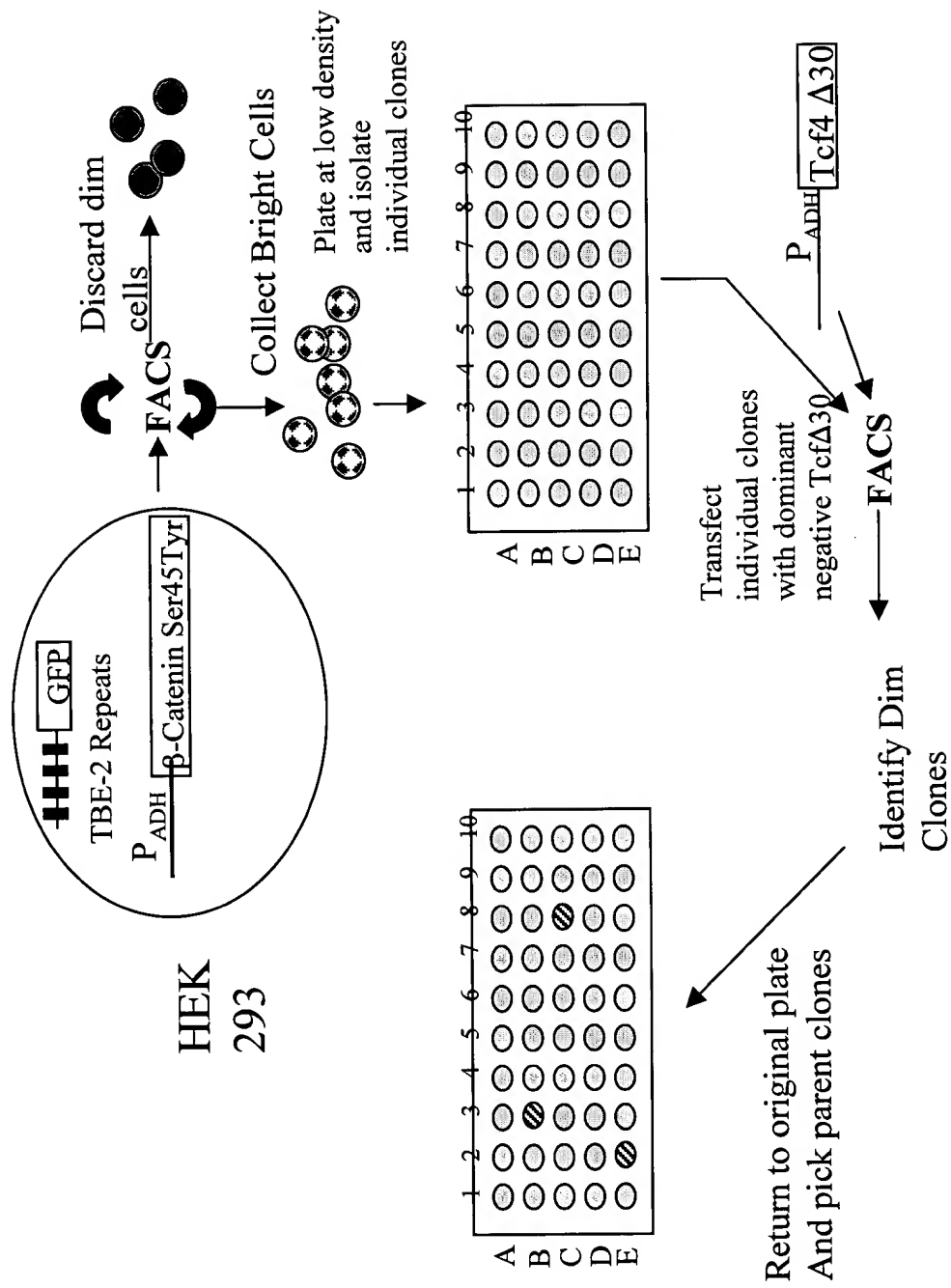


Figure 3

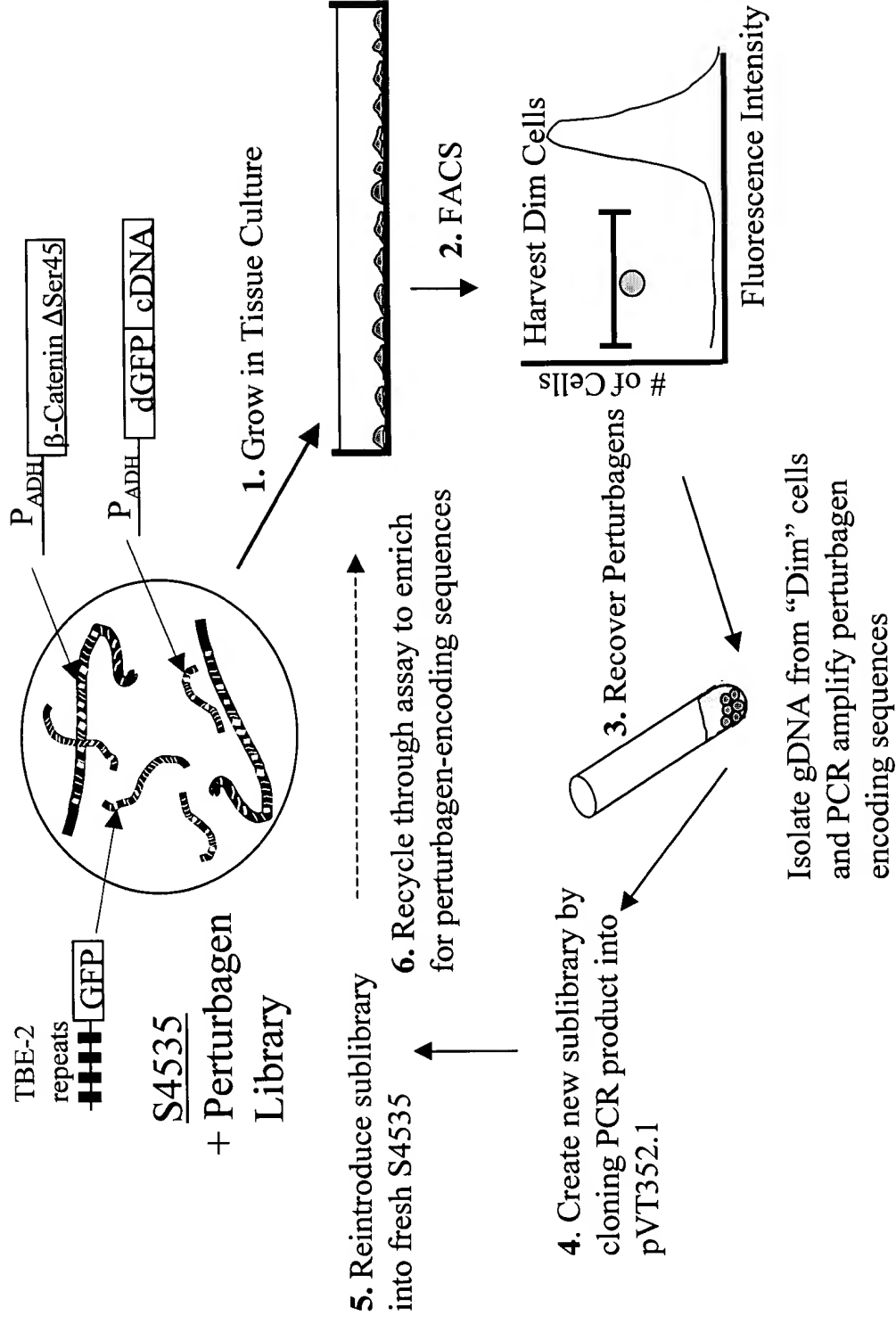


Figure 4

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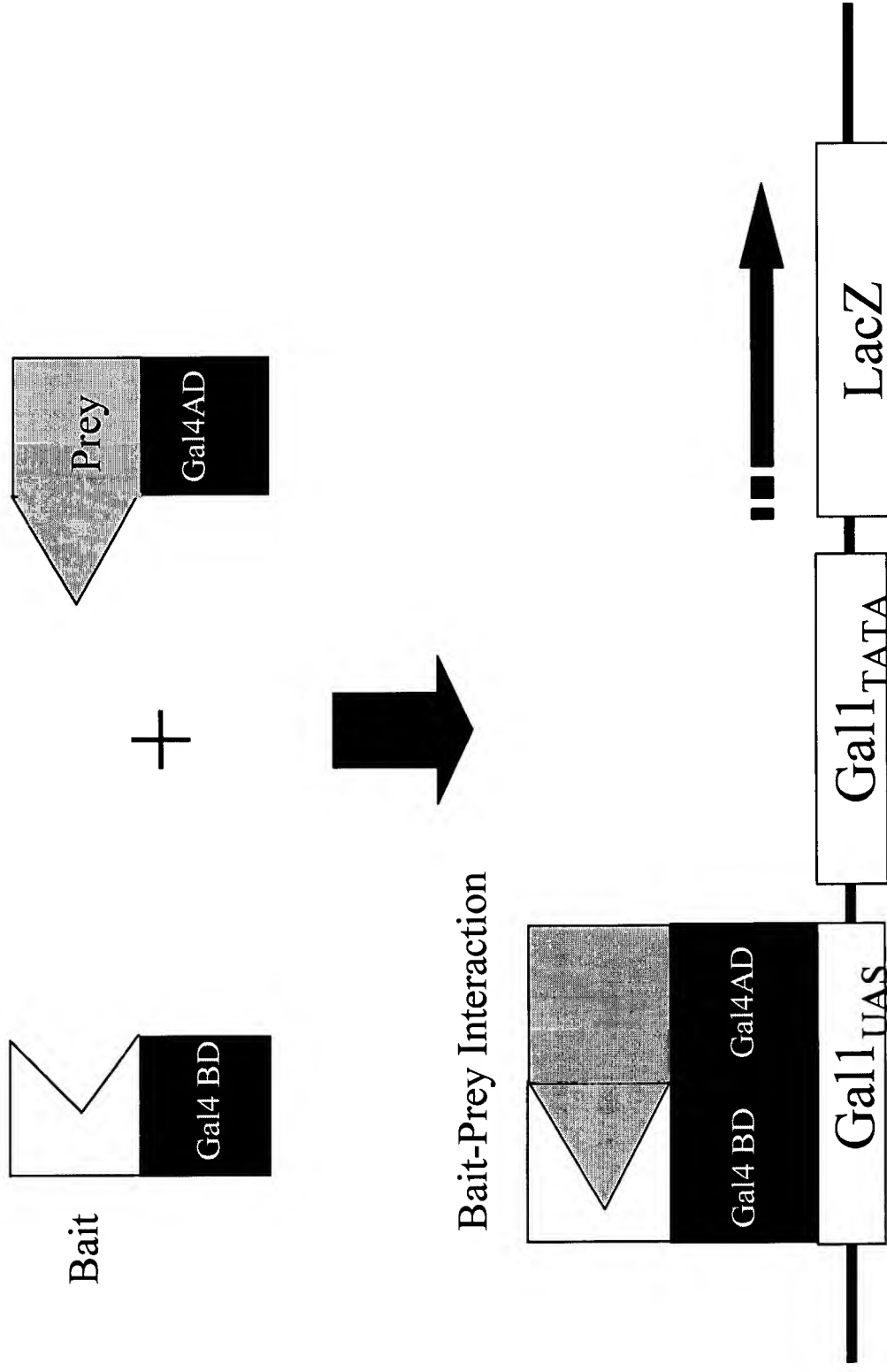


Figure 5

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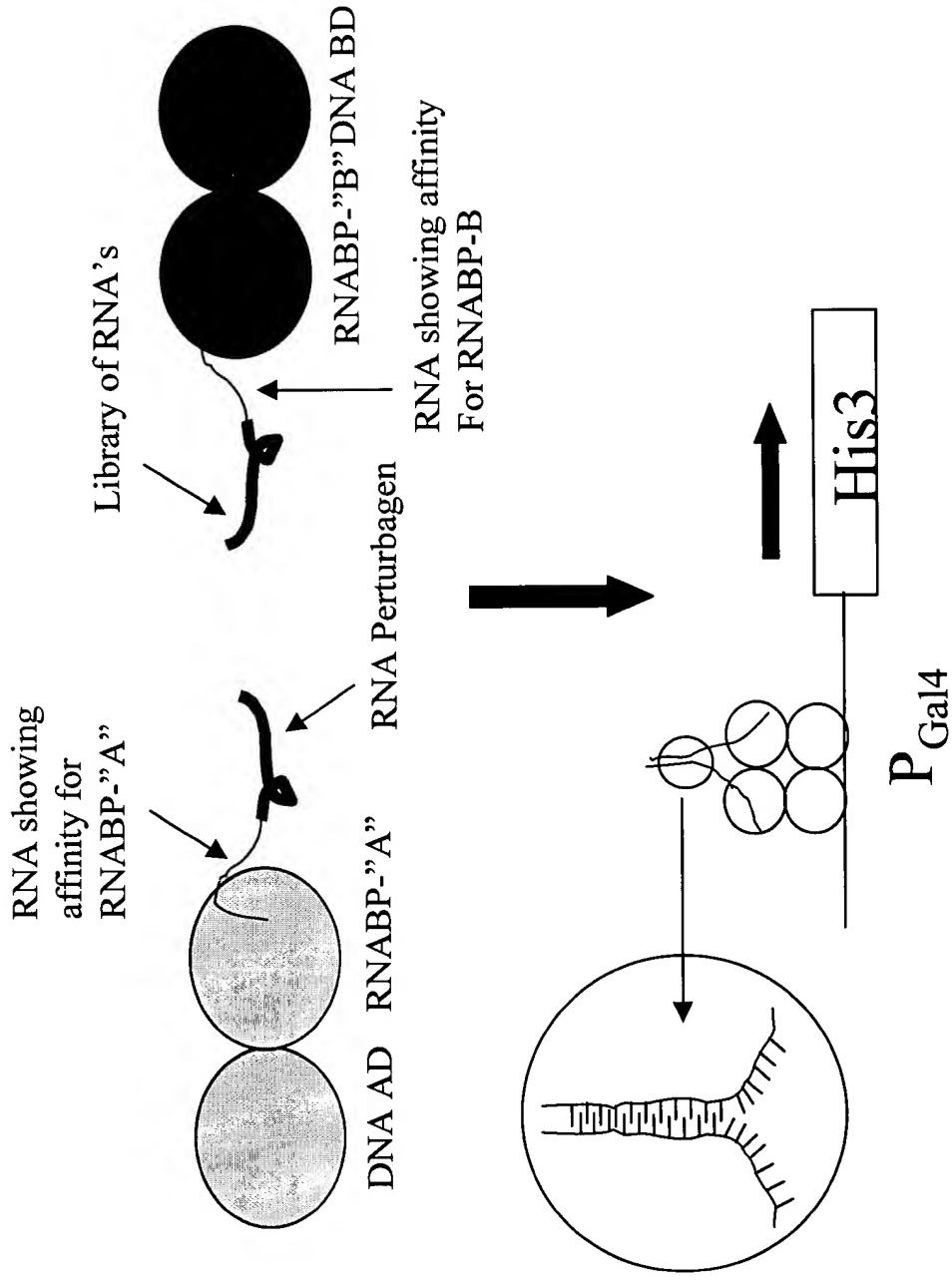


Figure 6

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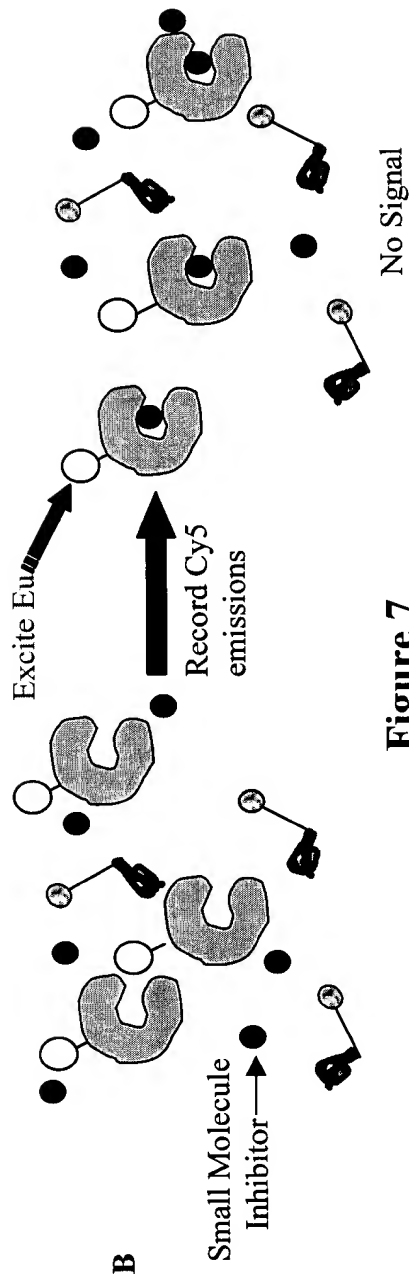
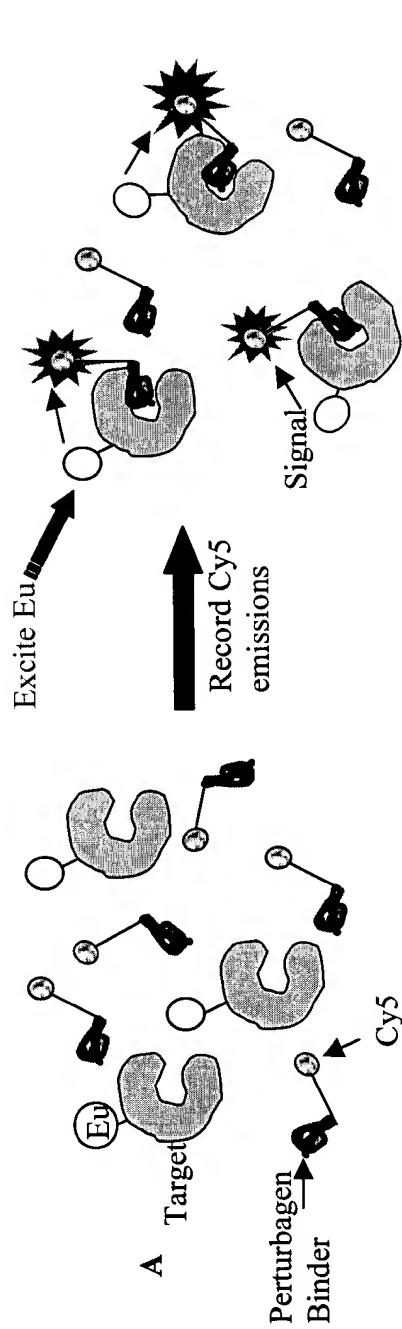


Figure 7

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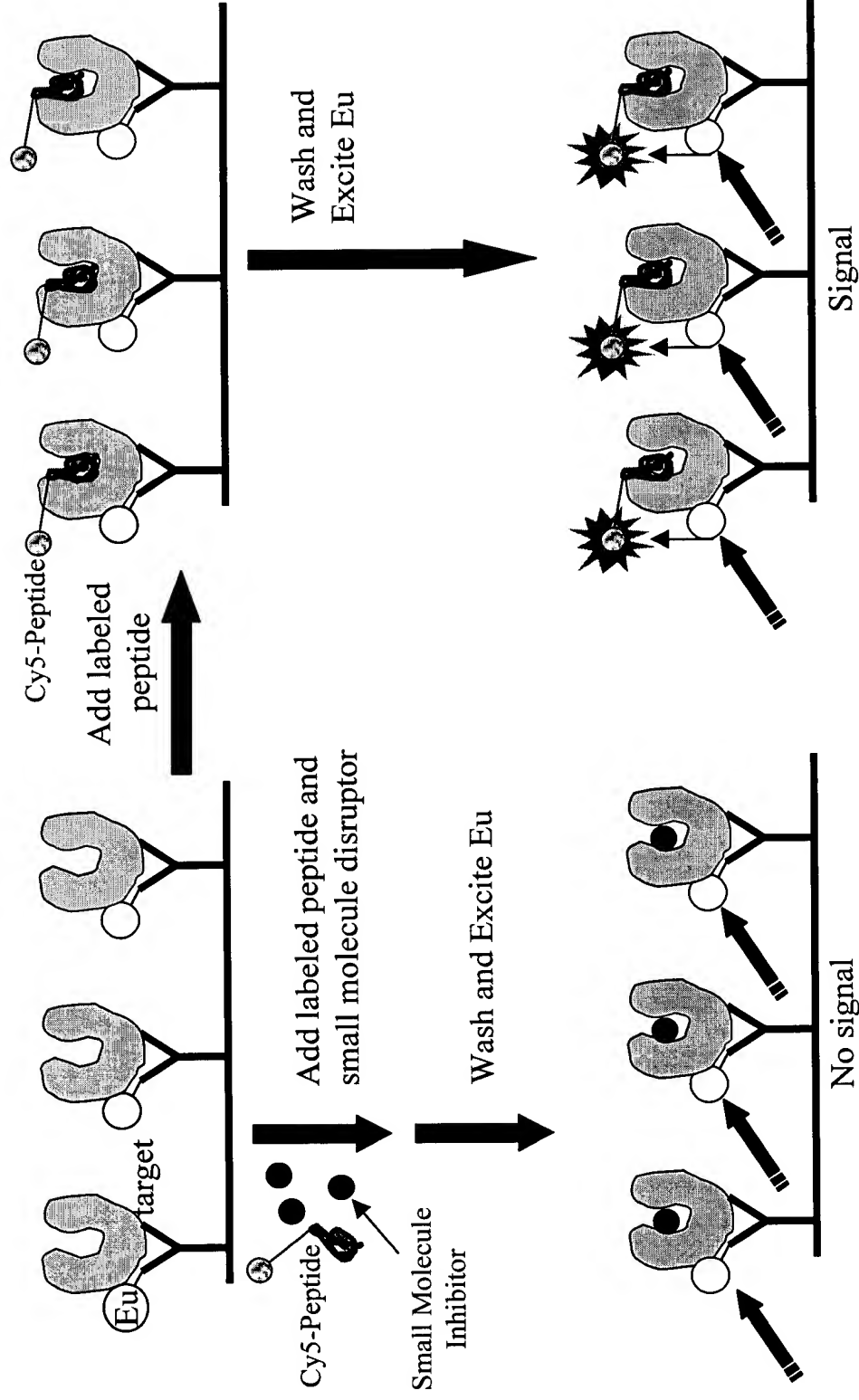


Figure 8



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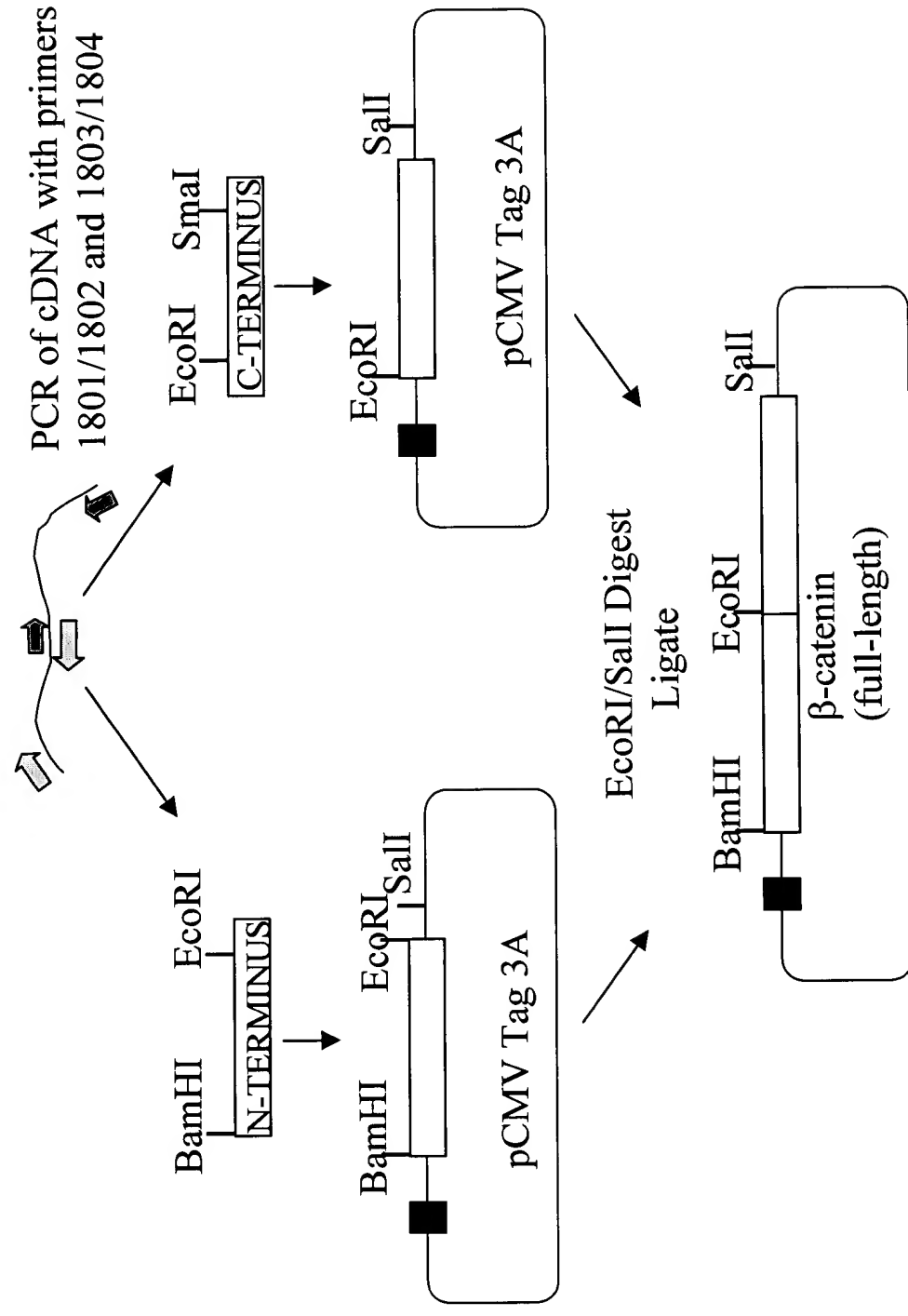


Figure 9

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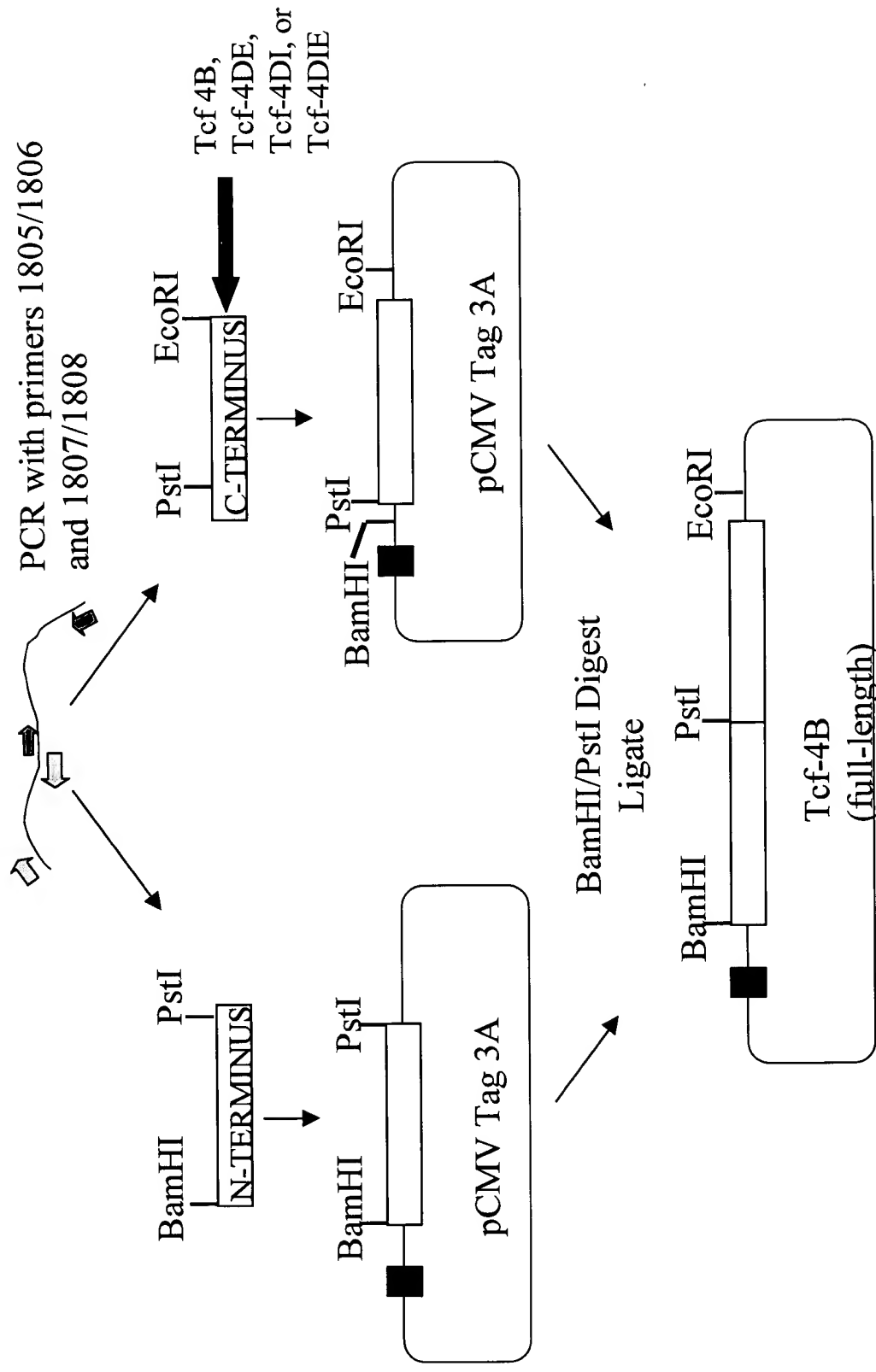


Figure 10

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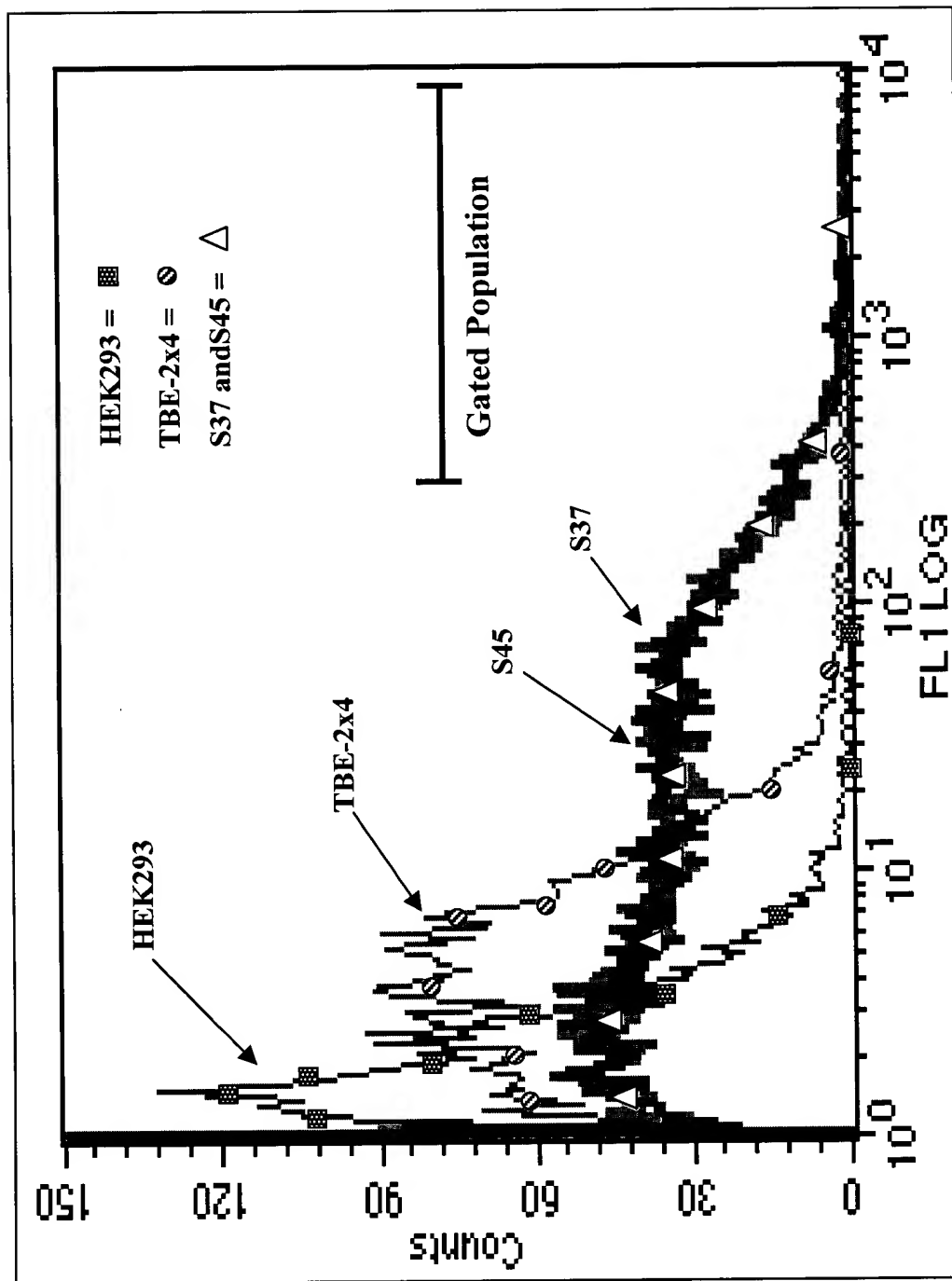


Figure 11

POST-20000

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(3)SY000006.LMD FL1 LOG singles

TBE2EGFP

X-Mean: 1.2

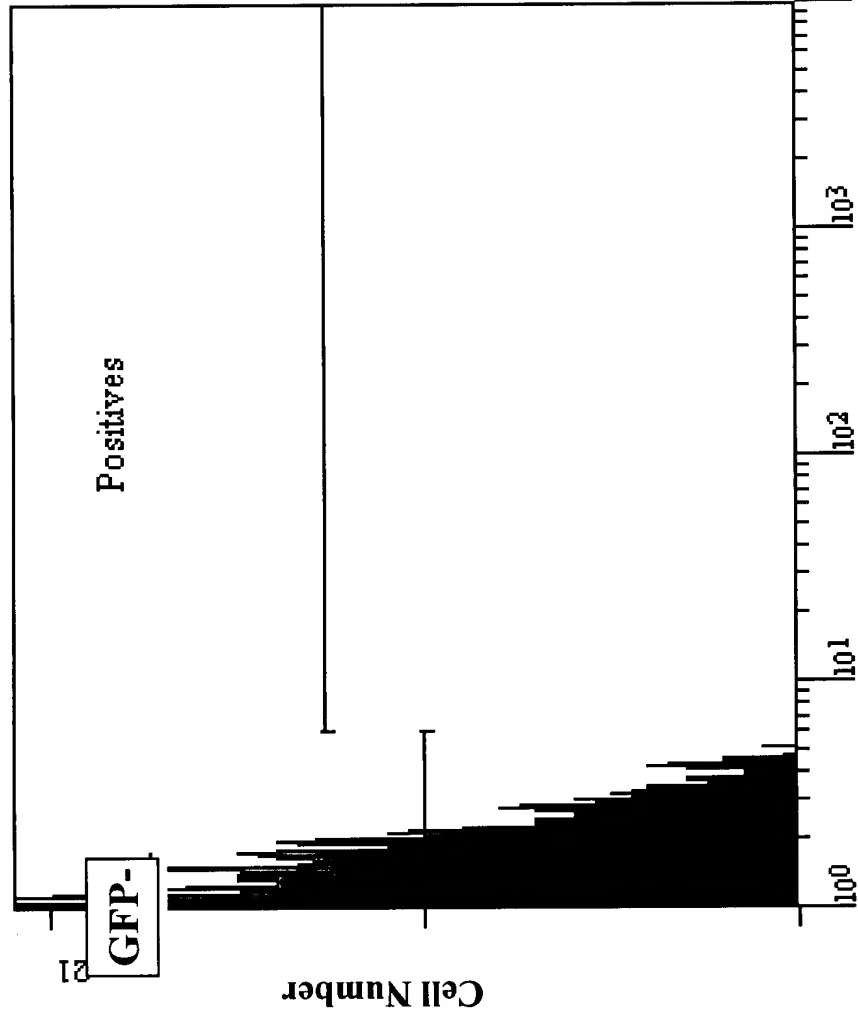


Figure 12A

FL1 LOG

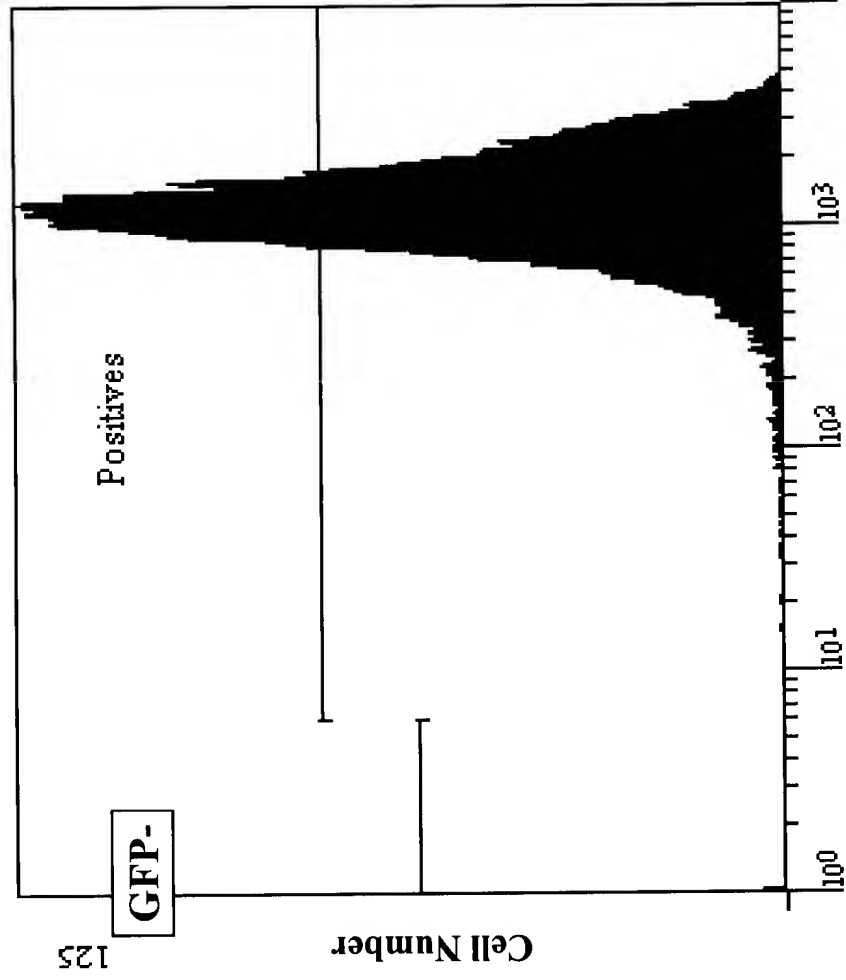
40947-240000

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(2) SY000027 LMD FL1 LOG singles

S45-35

X-Mean:1304.1



FL1 LOG

Figure 12B

FOSTF 2F60000

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(3):SY000028.LMD FL1 LOG Singles

+dGFPATcf4DI

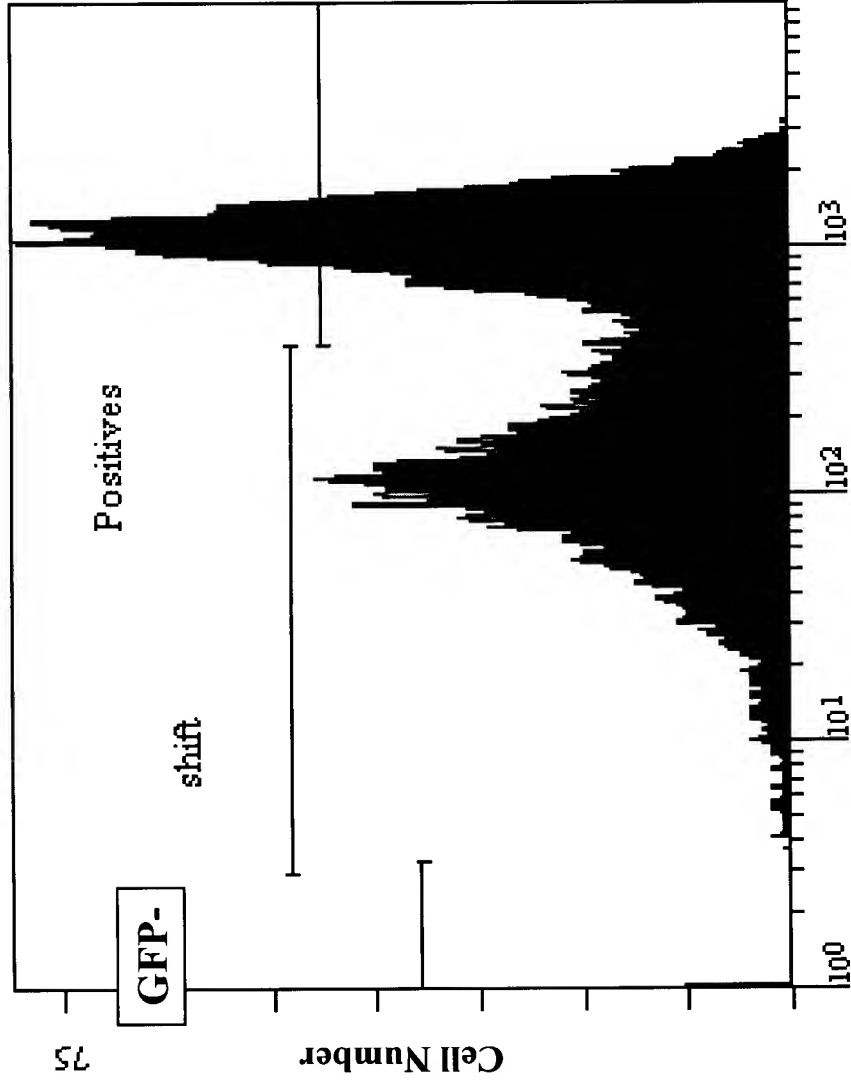


Figure 12C

FL1 LOG

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## CADHERIN V PERTURBAGEN

### DNA SEQUENCE

5' TTCCCTCTATGCGCAGGTGCAGAAAGCCACCGAGGCACGCGCCTGGGGCACAC  
GGAGGGCCCGGGAGATGGCAGCCATGATCGAGGTGAAGAAGGACGAGCGGA  
CCACGACGGCAGCGCCCCCTACGACACGCTGCACATCTACGGCTACGAGGG  
CTCCAAGTCCATAGCCAAGTCCCTCAGCTCCCTGGGCACCGACTCATCCGACTCT  
GACATGGATTACGACTTCCTTAACGACTGGGGACCCAGGTTTAAGATGCTGGCTG  
AGCTGTACGGCTCGGACCCCCGGAAGGAGCCA

### PEPTIDE SEQUENCE

PYGSRNVSKIKCCCNGLAFSLMHIEYALLAIMESMFISLGEQPTSLCTFQGPQGVL  
CPEPWVPSKPRGVLCHGLRFVWQGSLLPPFGTELA VPK

**Figure 13**

# CADHERIN VI PERTURBAGEN

## DNA SEQUENCE

GCGAAAAAA GAGCCTTTGA TCATTTCCAA AGAGGACATC AGAGATAACA  
 TTGTCAGTTA CAACGACGAA GGTGGTGGAG AGGAGGACAC CCAGGCTTTT  
 GATATCGGCA CCTGAGGAA TCCTGAAGCC ATAGAGGACA ACAAATTACG  
 AAGGACATT GTGCCCGAAG CCTTTTCCCT ACCCCGACGG ACTCCAACAG  
 CTCGCGACAA CACCGATGTC AGAGATTTC AATAACCAAAG GTTAAAGGAA  
 AATGACACGG ACCCCACTGC CCCGCCATAC GACTCCTTGG CCACTTACGC  
 CTATGAAGGC ACTGGCTCCG TGGCGGATTC CCTGAGCTCG CTGGAGTCAG  
 TGACCAACGA TGCAGATCAA GACTATGATT ACCTTAGTGA CTGGGACCT  
 CGATTCAAAA AGCTTGCAGA TATGTATGGA GGAGTGGACA GTGACAAAAGA  
 CTCCTAATCT GTTGCCTTTT TCATTTTCCA ATACGACACT GAAATATGTG  
 AAGTGGNTAT TTTCTTTATA TTTTACCCAC TACCNCGAAA

## PEPTIDE SEQUENCE

PRKKEPLISXXDIXDNIVSYNDEGGGEEDTQAFDIGTLRNPEAIEDNKLRRDIV  
 PEALFLPR

Figure 14



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## CADHERIN XI

### DNA SEQUENCE

TAGACCTGGGCTCCGGCCAGCGCCCAACAGCGTGGATGTCGATGACTTCATCAA  
CACGAGAAACACAGGAGGCAGACAAATGACCCACGGCTCCTTATGACTCCAT  
TCAAACTCTACGGTTATAAAGGCAGGGGCTCAGTGGCCGGTCCCTGAGCTCCCT  
AGAGTCGGCCACCACAGATTCAGACTTGGACTATGATTATCTACAGAACTGGGG  
ACCTCGTTTTAAGAACTAGCAGATTTGTATGGTTCCAAAGACACTTTTGATGAC  
GATTCTTAACAATAACGATACAAATTTGGCCTTAAGAACTGTGTCTGGCGTTCTC  
AAGAATCTAGAAGATGTGTAAACAGGTATTTTTTAAATCAAGGAAAGGCTCAT  
TTAAACACAGGCAAAAGTTTACAGAGAGGATACATTTAATAAACTGCGAGGACA  
TCAAAGGGTAAA

### PEPTIDE SEQUENCE

PRPGLRPAPNSVDVDDFINTRIQEADNDPTAPPYDSIQIYGYEGRGSVAGSLSSLES  
ATTDSDLDYDYLQNWGPRFKKLADLYGSKDTFDDDS

Figure 15

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singles FL1 LOG

# Cadherin V

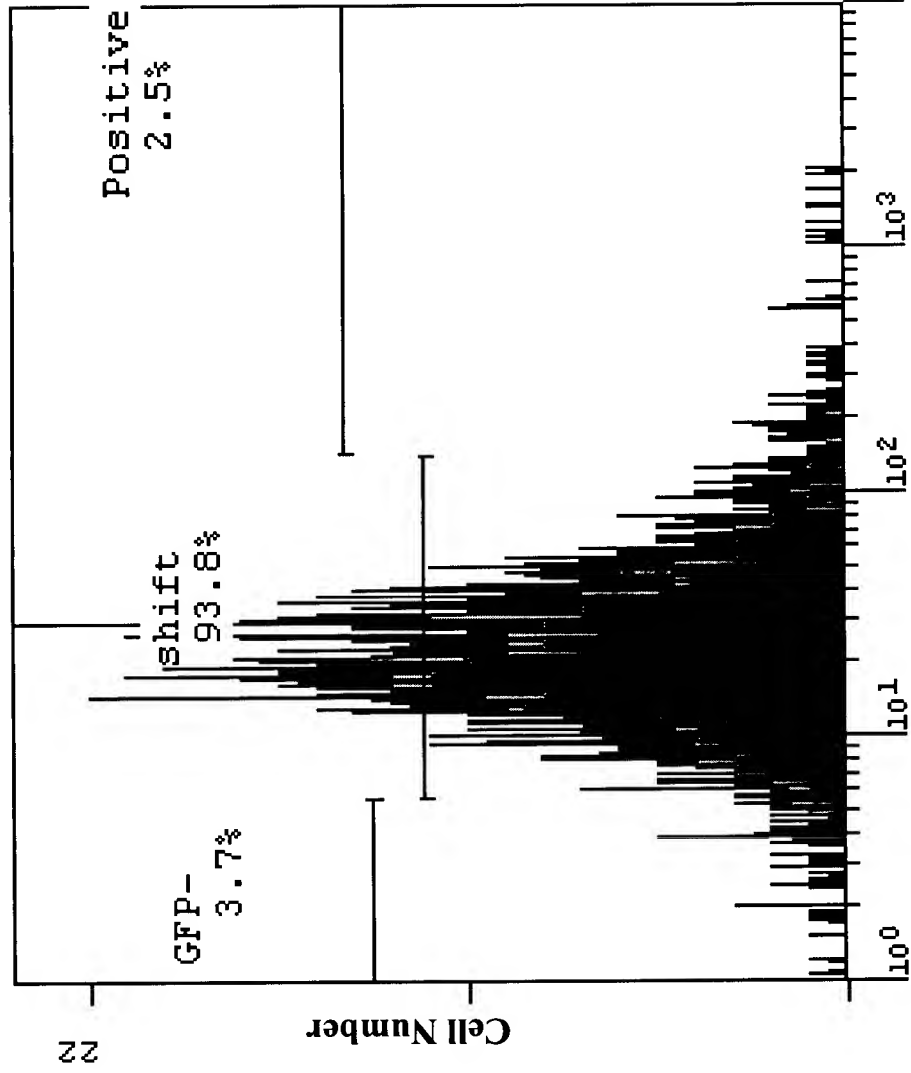


Figure 16

FL1 LOG

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# Dead Cell Number

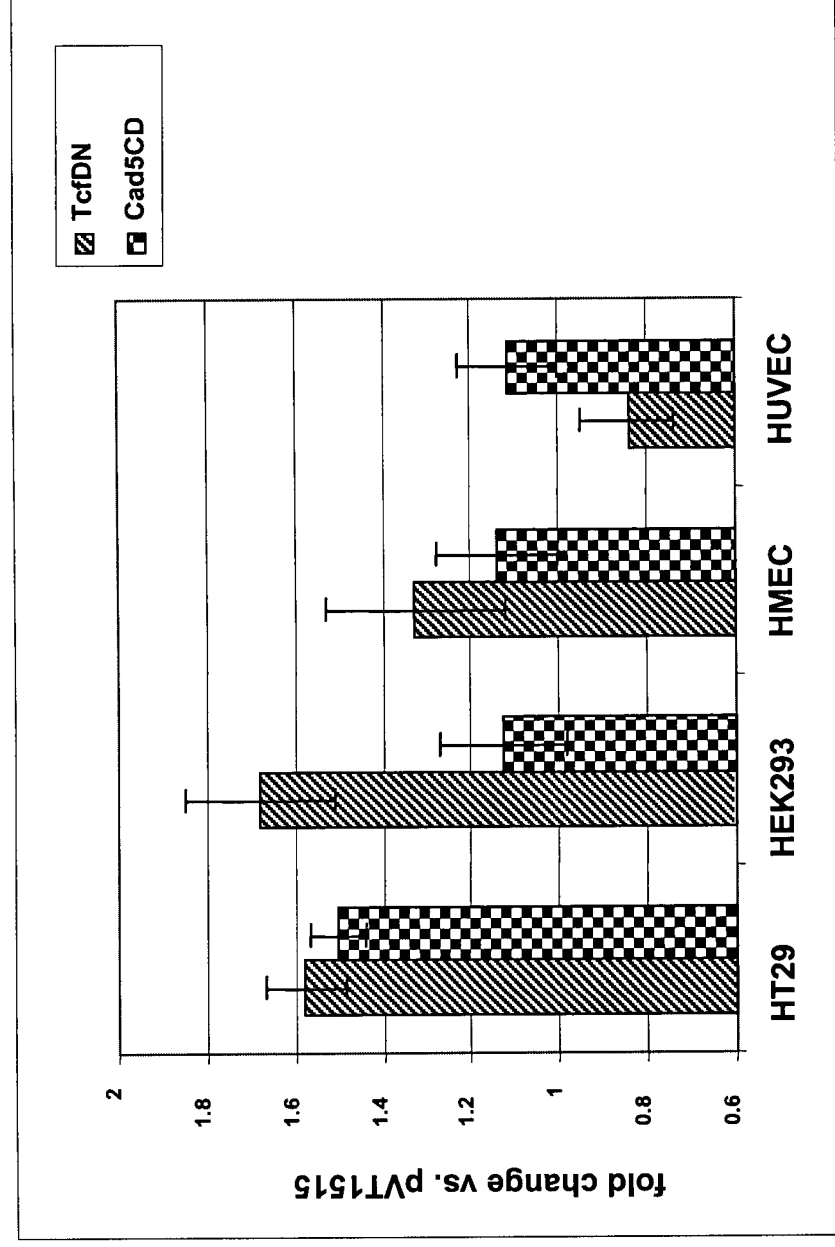


Figure 17

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# Total Cell Number

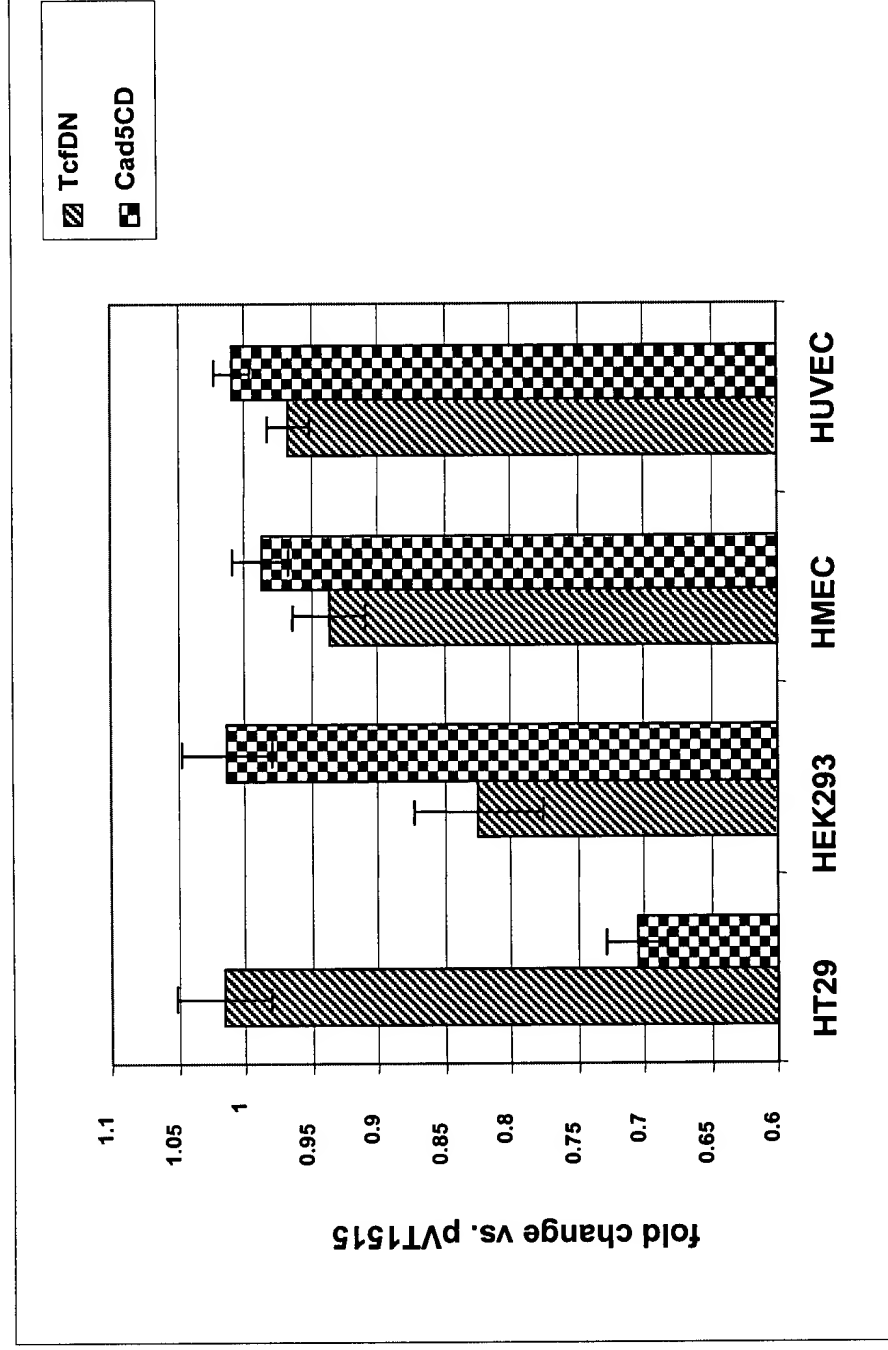


Figure 18

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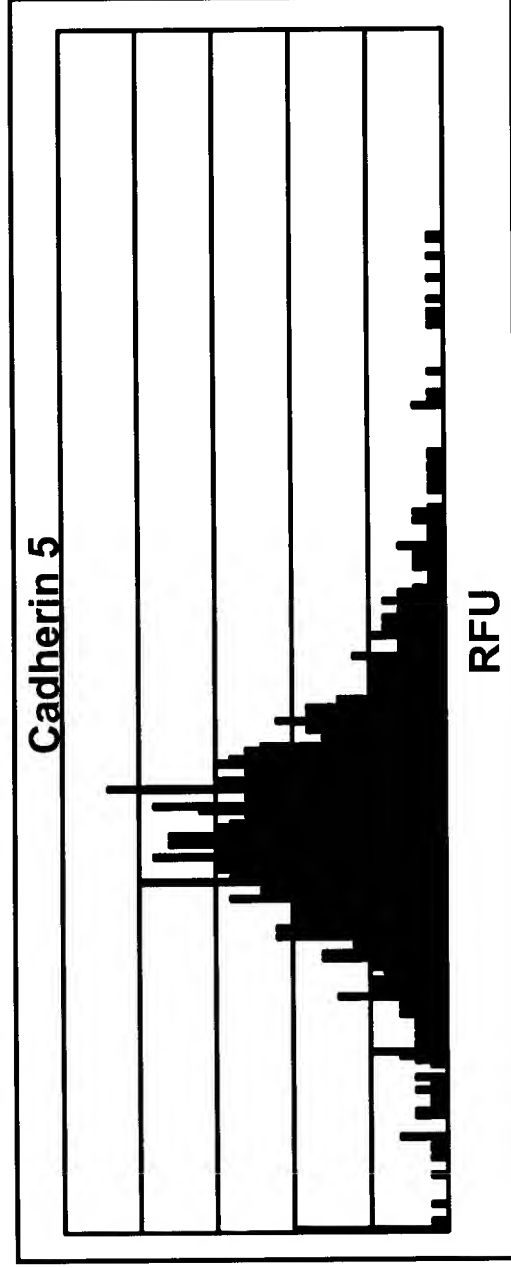
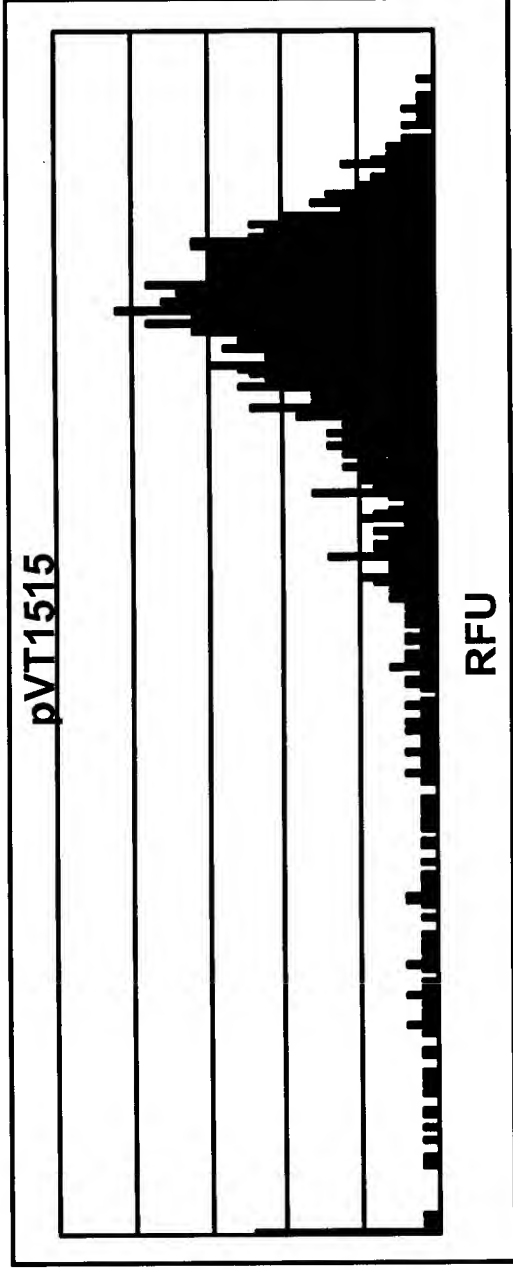


Figure 19

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Cad5CD/TcFDN

Cad5CD	TcFDN	Cad5CD	TcFDN	Clone ID	Accession No.	GeneName
Ratio	Ratio	z	z			
-2.2	-1.8	-7.3	-5.5	3580257	AP001708	genomic DNA, chromosome 21q
-1.5	-1.4	-5.5	-4.5	179196	AK025459	cDNA: highly similar to tra1 homologue of murine tumor rejection antigen gp96.
-1.9	-1.7	-5.4	-4.4	4291484	M55536	glucose transporter pseudogene.
-1.6	-1.3	-5.2	-3.7	1992945	AF016052	zinc finger protein ZNF191
-1.8	-1.5	-4.5	-3.3	23770	X57351	1-8D gene from interferon-inducible gene family.
-1.4	-1.7	-4.1	-6.8	459372	AF255303	membrane-associated nucleic acid binding protein
-1.3	-1.4	-3.8	-4.3	5188302	M26708	prothymosin alpha (ProT-alpha)
-1.5	-1.6	-3.7	-4.9	5046235	AAC72274	ZO-3
-1.3	-1.3	-3.6	-3.2	3592429	CAA26743	E1b 55k protein (transformation)
-1.6	-2	-3.5	-5.0	2834343	U52682	lymphocyte specific interferon regulatory factor 4 (LSIRF/IRF4)
-1.3	-1.4	-3.3	-4.5	2155121	X79535	beta tubulin
-1.3	-1.3	-3.3	-3.8	5003513	X54134	protein tyrosine phosphatase epsilon.
-1.4	-1.7	-3.3	-5.2	2833609	X05908	lipocortin.
-1.2	-1.2	-3.2	-3.0	2552381	M36981	putative NDP kinase (nm23-H2S)
-1.5	-1.6	-3.2	-3.3	2822027	AB002341	KIAA0343
1.3	1.3	3.2	3.4	4062068	AF107885	Ch 14q24.3, transforming growth factor-beta 3 (TGF-beta 3), unknown genes.
1.3	1.4	3.4	3.6	4721478	AB003103	26S proteasome subunit p55
1.4	1.3	3.7	3.0	3865578	U86282	olfactory receptor (OR7-86) pseudogene

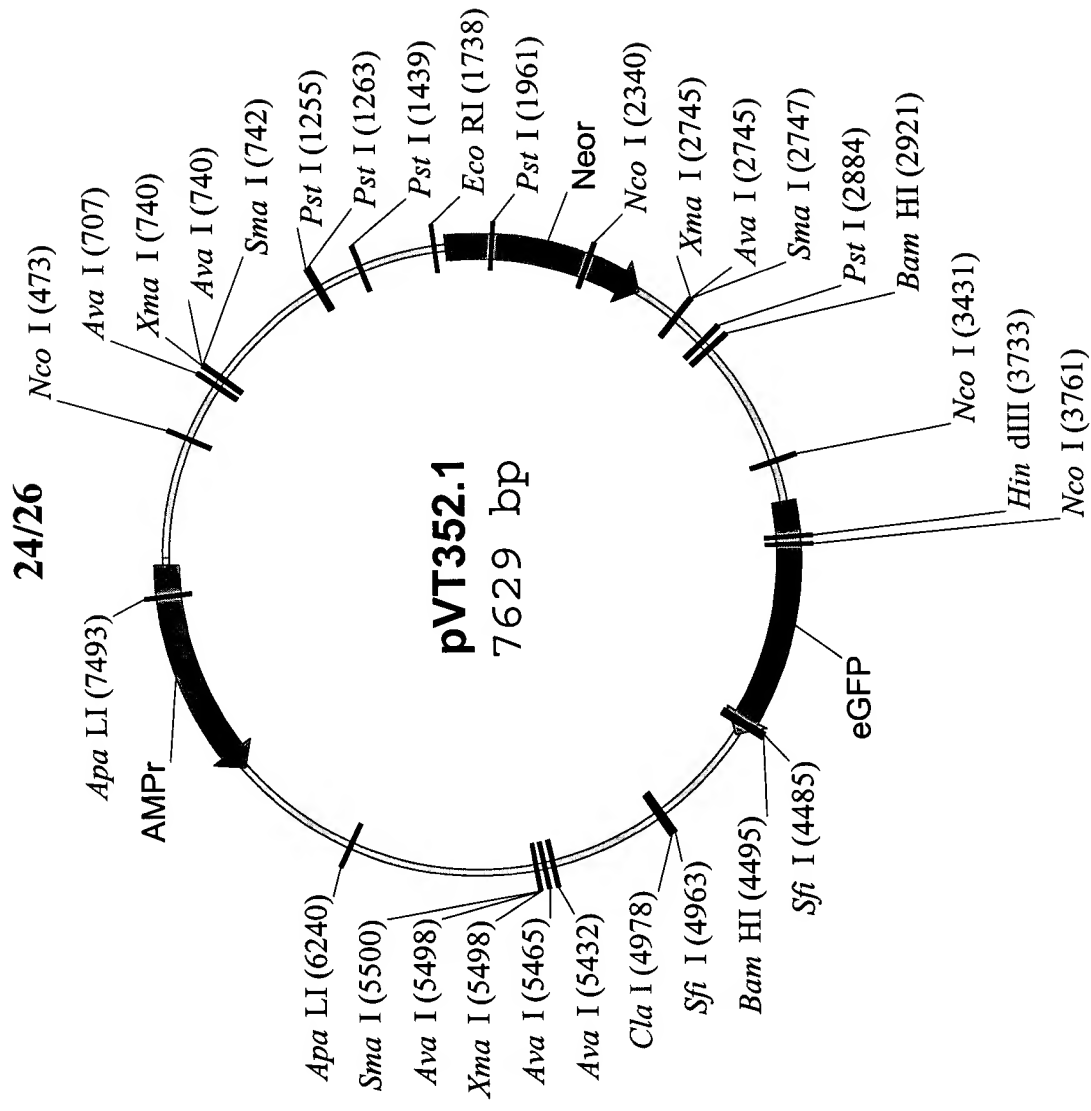
Figure 20

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Cad5CD

Ratio	Ratio	Z	Z	Clone ID	Accession No.	GeneName
-2.3	-1.4	-4.4	-1.8	5047895	AF177394	dickkopf-1 (DKK-1)
-2.2	-1.5	-4.2	-2.2	3050732	AF078165	axin-2
-1.4	-1.1	-3.7	-1.6	380006	M29064	hnRNP B1.
-1.3	-1.2	-3.5	-2.2	1511778	M73554	bcl-1 (cyclin D1)
-1.6	-1.5	-3.2	-2.7	2120743	AK023638	cDNA FLJ13576 fis.
-1.3	-1.2	-3.1	-2.9	4163444	M26697	nucleolar protein (B23)
-1.7	-1.6	-3.1	-2.6	1658215	X61118	TTG-2 cysteine rich protein with LIM motif.
-1.7	-1.4	-3.1	-2.0	1921238	M20681	glucose transporter-like protein-III (GLUT3)
-1.3	-1.1	-3.0	-1.4	2135733	AY007131	clone CDABP0045
-1.6	-1.4	-3.0	-2.3	4760384	AF155661	pyruvate dehydrogenase (PDH)
-1.6	-1.5	-3.4	-2.9	968676	S53354	B-cell activation protein=B-G antigen IgV domain homolog
1.3	1.1	3.1	1.0	5207613		Incyte EST
1.3	1.3	3.1	2.4	4879313	AP001676	genomic DNA, chromosome 21q
1.6	1.5	3.1	2.3	4271973	AF125348	caveolin 1 (CAV1)
1.4	1.2	4.1	2.4	2893021	AP001700	genomic DNA, chromosome 21q

Figure 21



**Figure 22**



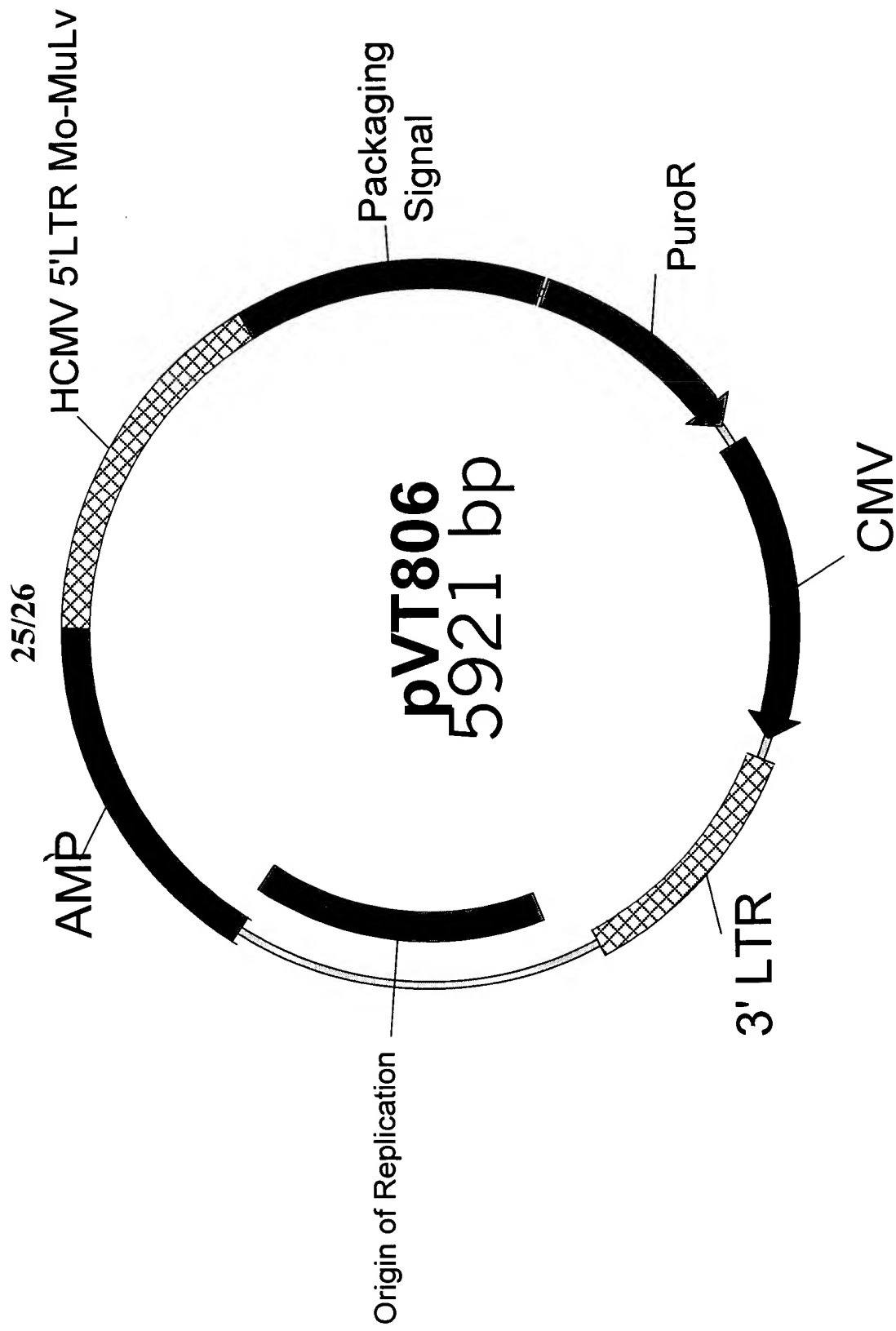


Figure 23

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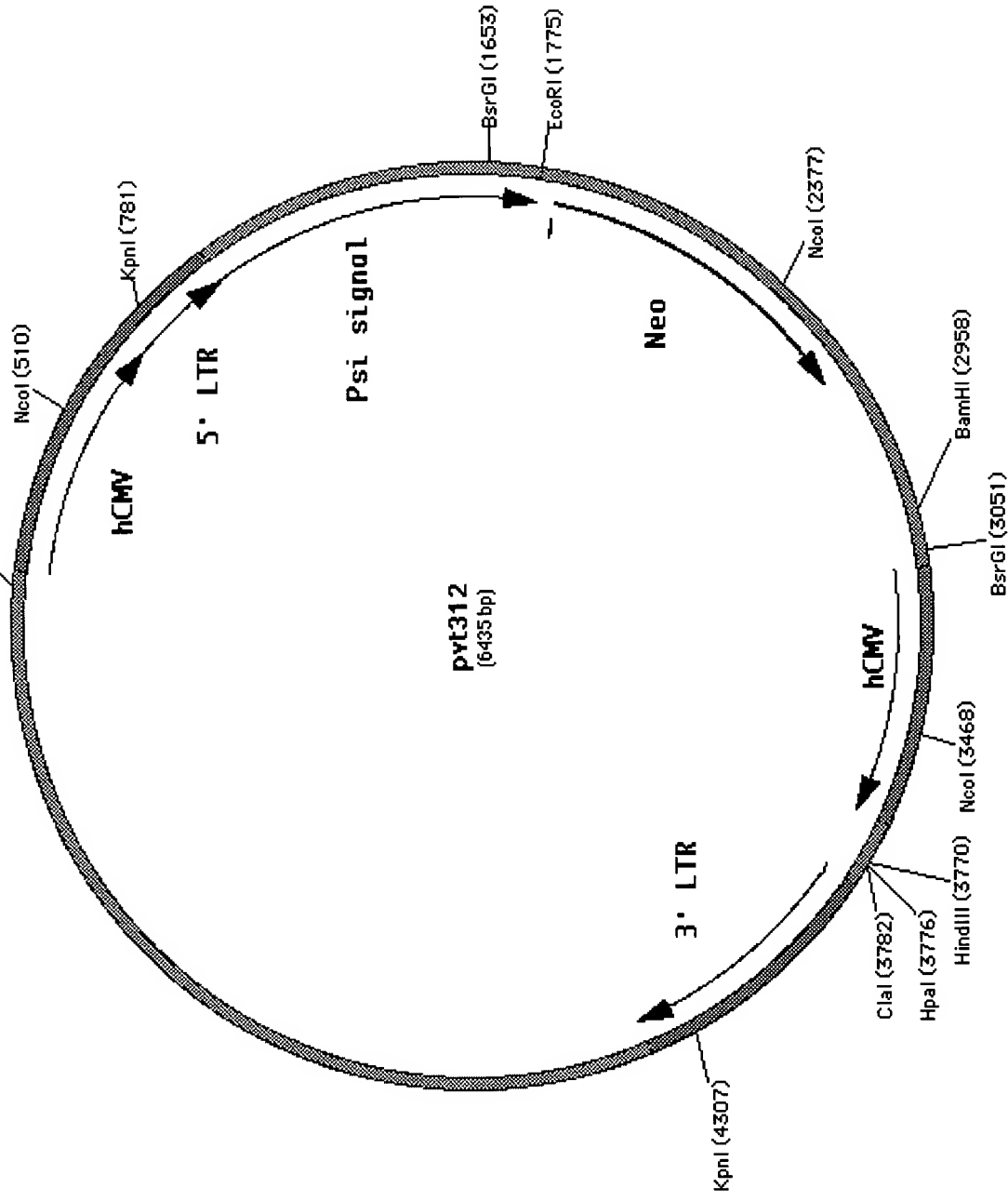


Figure 24